
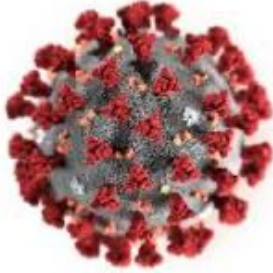




GLST 287:

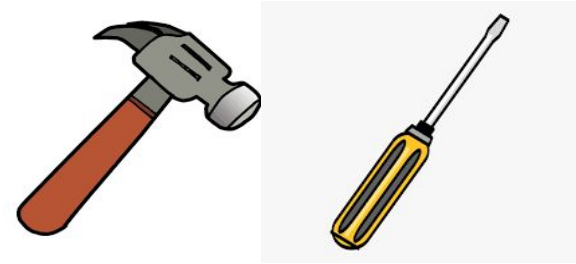
The Science of COVID-19 Part I: The What, Where, and How of Coronaviruses
Evan Eskew, Ph.D. and Shannon Seidel, Ph.D.

Humans vs SARS CoV-2

		
Genome?	3,000,000,000 bases pairs, double-stranded DNA	29,900 bases, single-stranded RNA
Genes?	~20,000-30,000	~10
Living?	Yes	Depends on your definition of living...

What is a living thing?

Biologists have historically thought about this question in two main ways: **STRUCTURE** and **FUNCTION**



Stop and think: What FUNCTIONS of living things can you think of?

Enter your answer in the Chat window on Zoom

Some FUNCTIONS of living things include:



STRUCTURES of living things

Cells!

Primary way of defining life after introduction of the microscope

Basis of Cell Theory

- Organisms are made up of one or more cells
- Cells are the basic unit of life

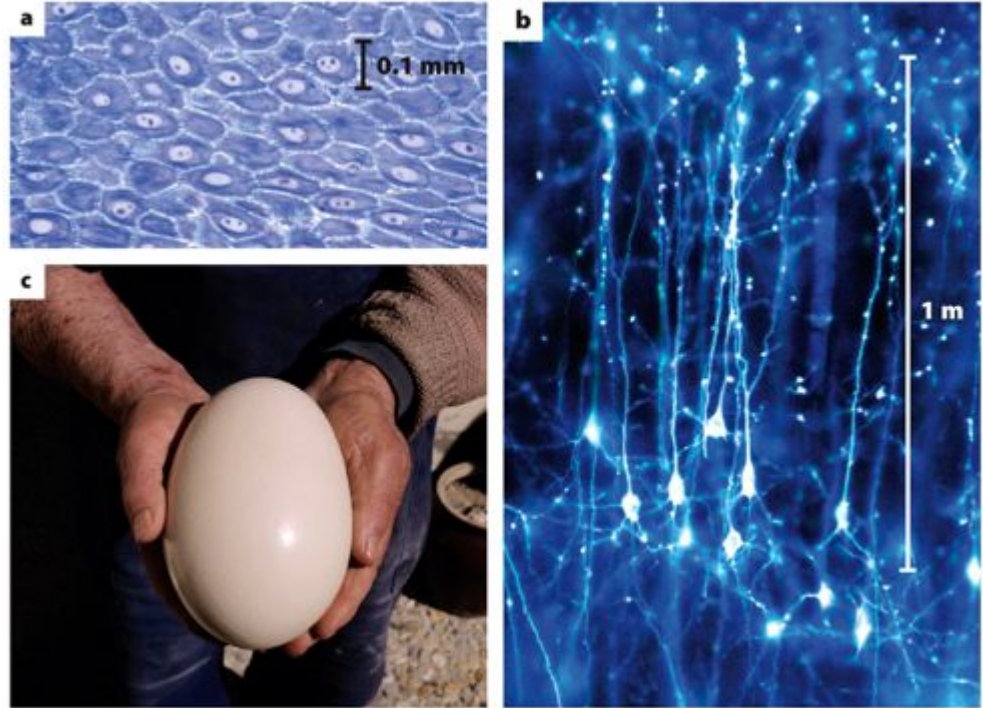


Figure 1.11
Biology: How Life Works
© 2014 W. H. Freeman and Company

Are viruses alive according to Cell Theory?

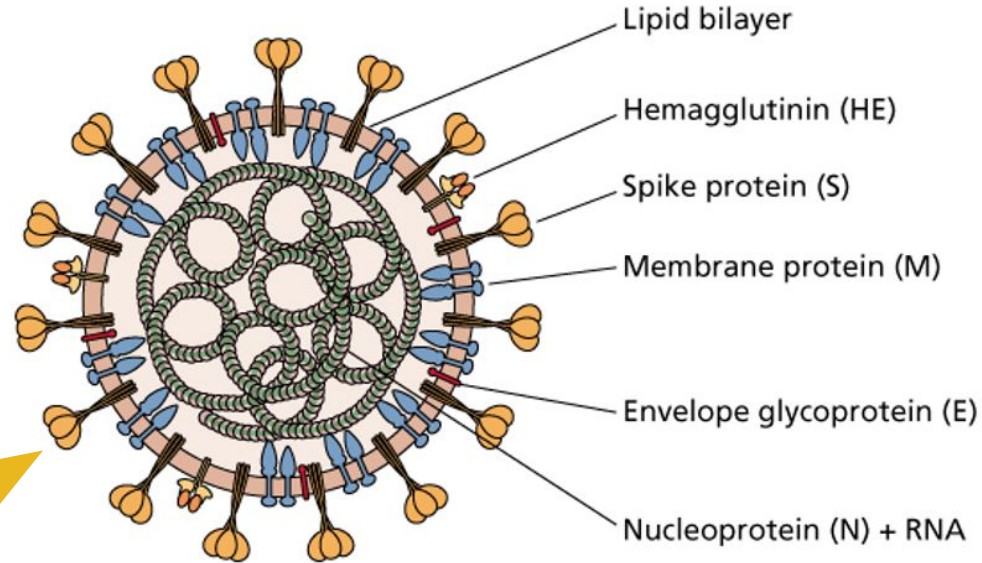
No. Viruses are not made of cells.

Viruses contain

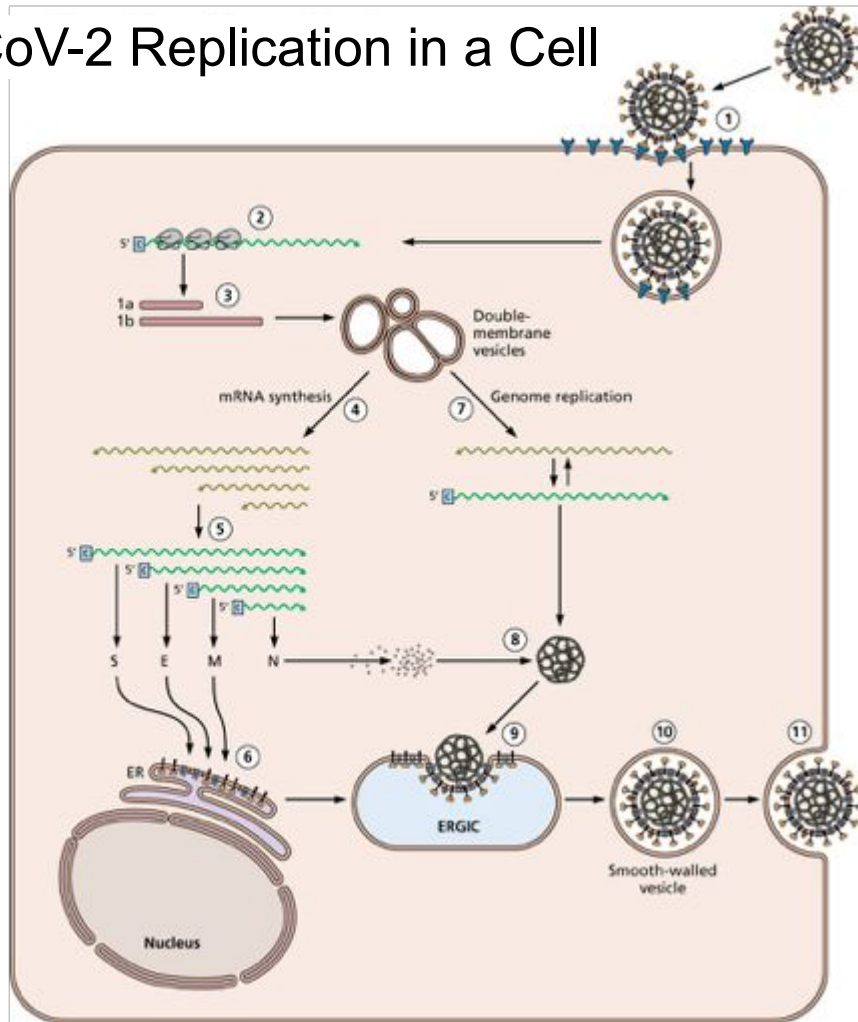
- 1) a genome (DNA or RNA)
- 2) protein coat
- 3) maybe a lipid bilayer

Yet! Viruses are more diverse than life itself.

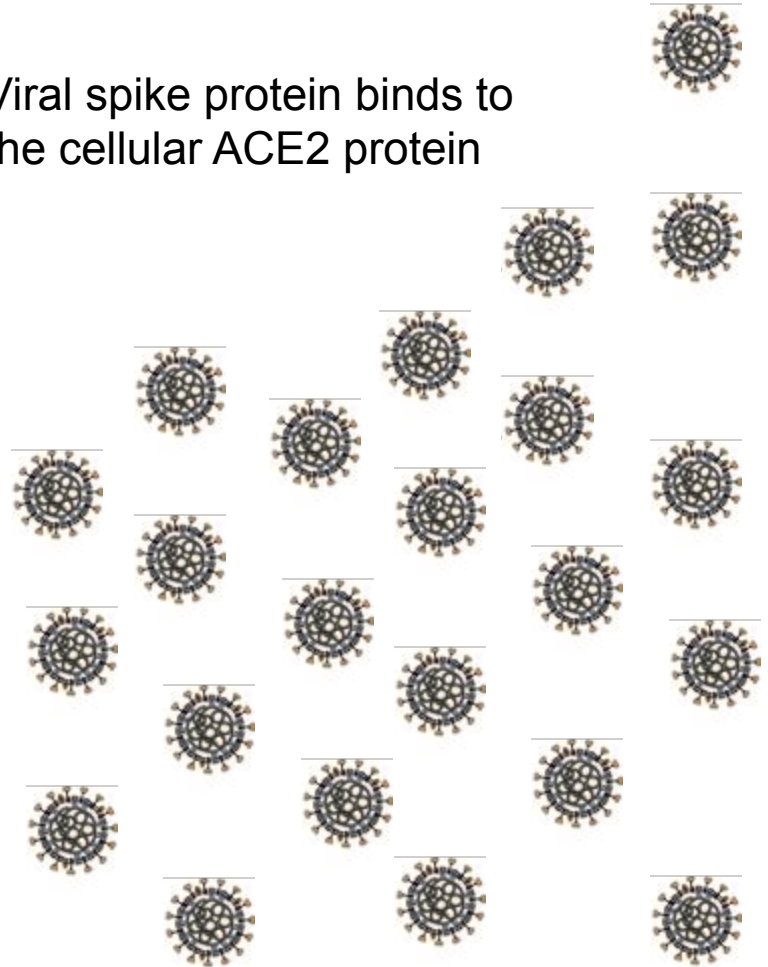
Spike Protein on the surface of the cell binds the host cell receptor



SARS CoV-2 Replication in a Cell



Viral spike protein binds to the cellular ACE2 protein



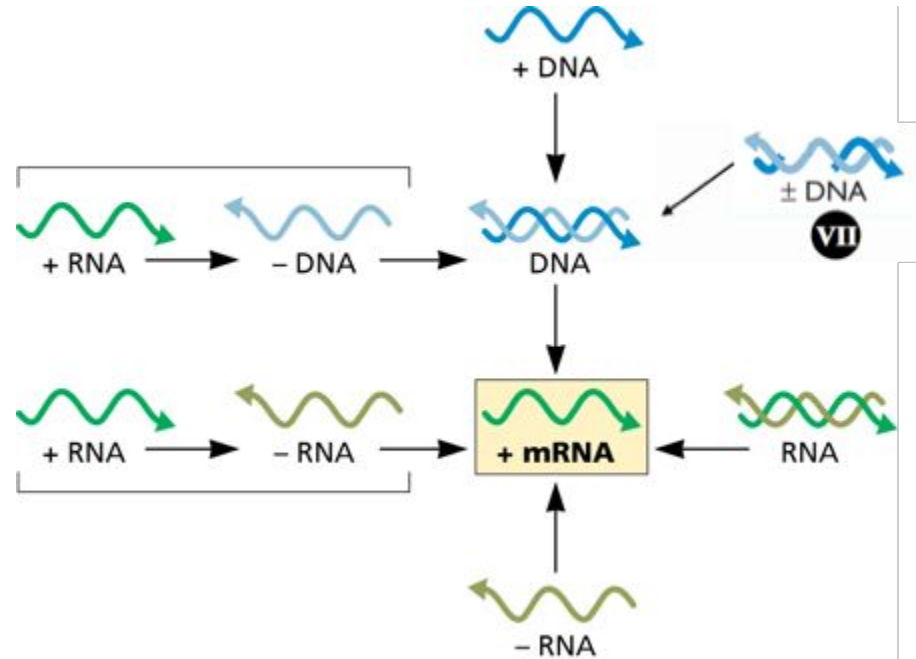
Living things

All have a double stranded DNA genome.



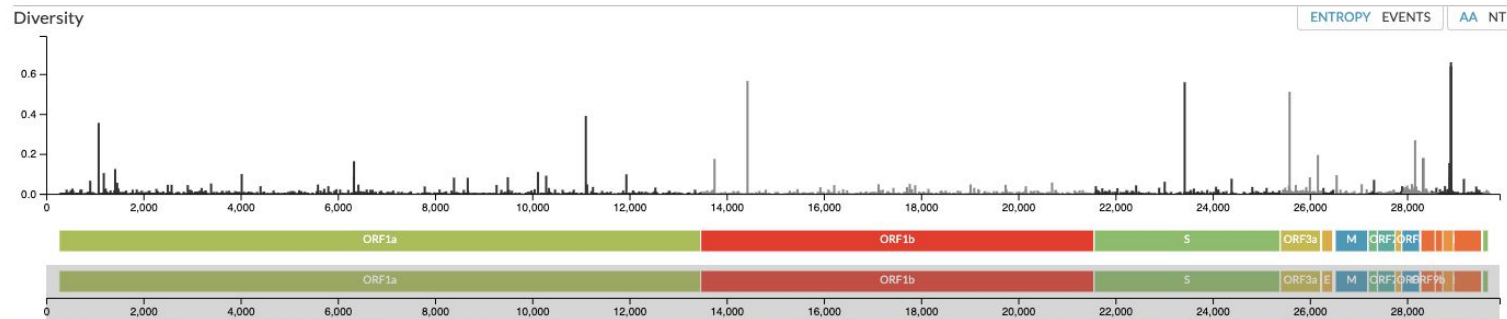
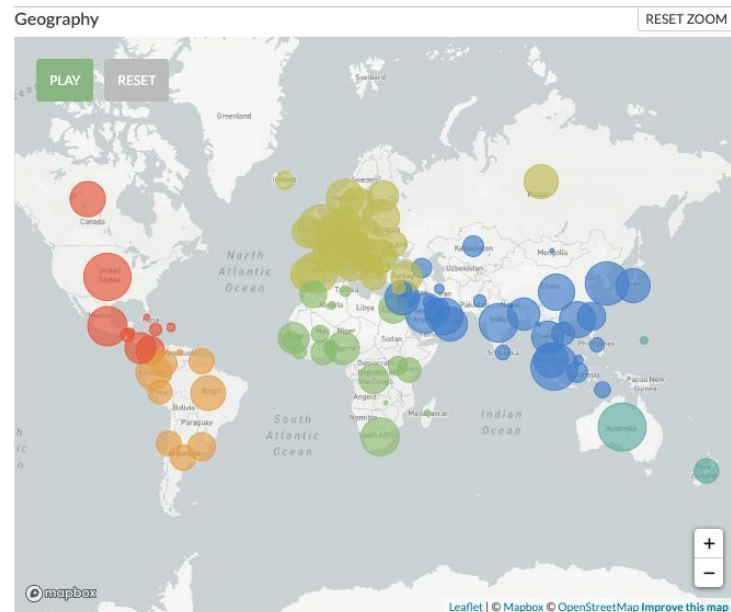
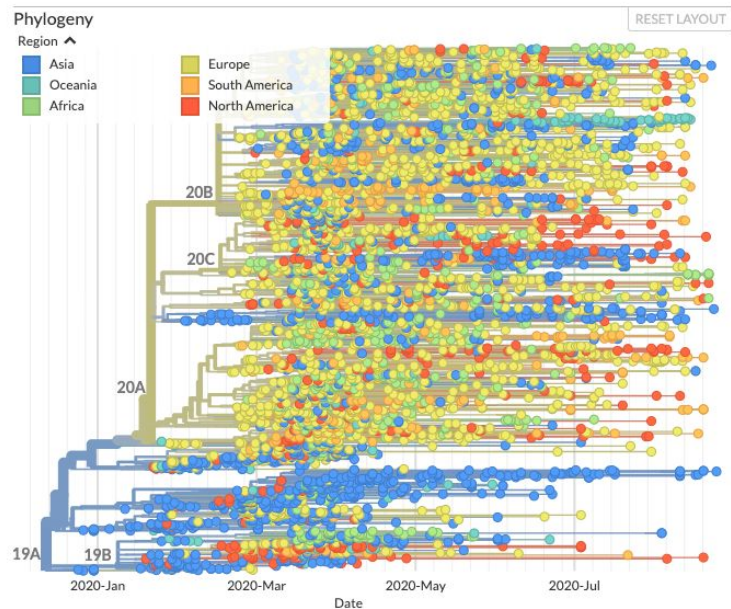
Viruses

Have many different types of genomes!



Nextstrain.org - Genomic Epidemiology of SARS CoV-2

Showing 4417 of 4417 genomes sampled between Dec 2019 and Aug 2020.





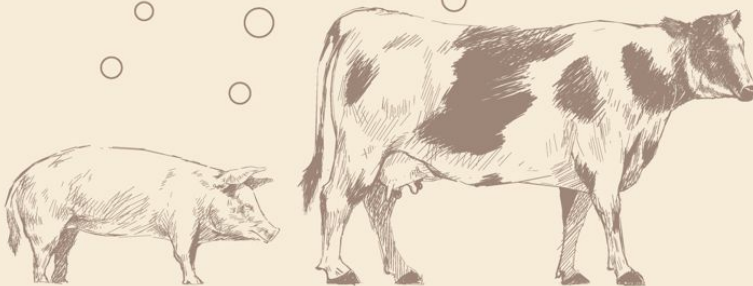
Brainstorm ways in which a virus could spill over from animals to people. In other words, how might a virus get from animals to people?

HOW ZOOONOTIC DISEASES are transmitted



Vector-born disease

Air-born/water-born disease



Proximity
or
direct contact
to animals



Food-born



Direct Contact



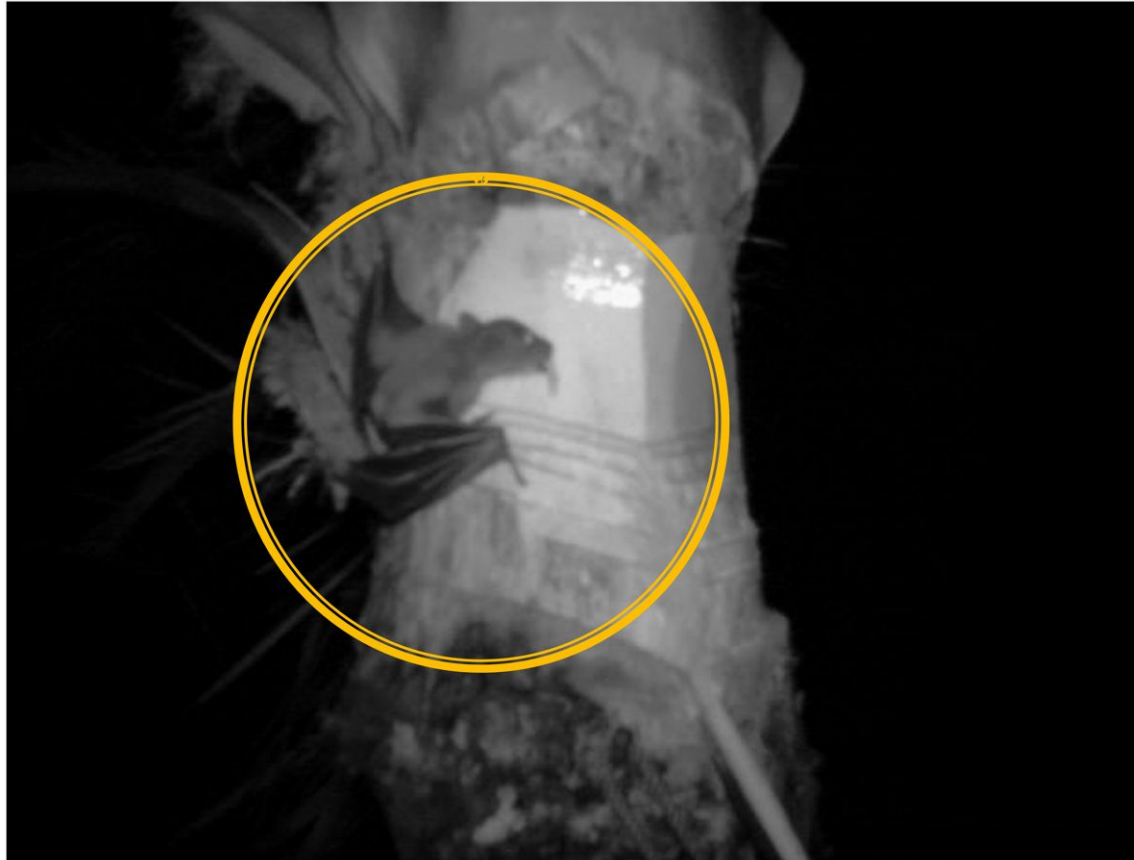
Food-Related



Indirect Contact (e.g., date palm sap)



Indirect Contact (e.g., date palm sap)

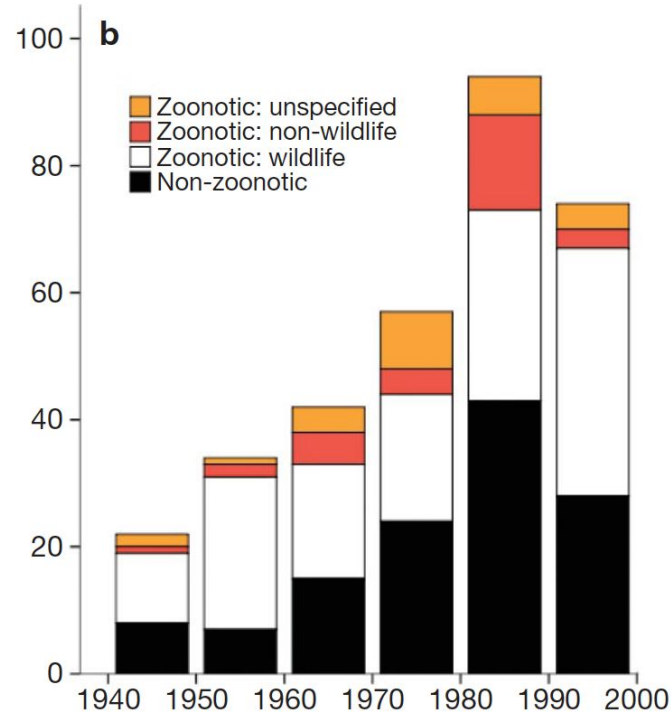


Indirect Contact (e.g., bat guano harvest)



Global trends in emerging infectious diseases

Kate E. Jones¹, Nikkita G. Patel², Marc A. Levy³, Adam Storeygard^{3†}, Deborah Balk^{3†}, John L. Gittleman⁴
& Peter Daszak²



Business

Deadly Virus Finds a Breeding Ground in China's Food Markets

Bloomberg News

January 20, 2020, 1:00 PM PST *Updated on January 20, 2020, 8:08 PM PST*



Wuhan seafood market may not be source of novel virus spreading globally

By [Jon Cohen](#) | Jan. 26, 2020 , 11:25 PM

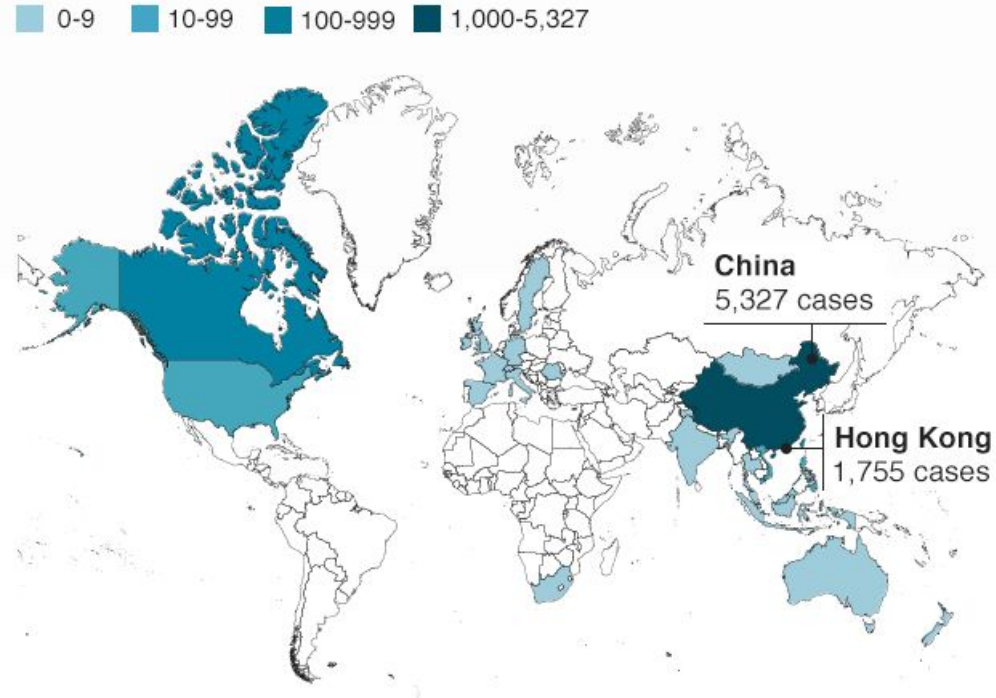
As confirmed cases of a novel virus surge around the world with worrisome speed, all eyes have so far focused on a seafood market in Wuhan, China, as the origin of the outbreak. But a description of the first clinical cases [published in *The Lancet*](#) on Friday challenges that hypothesis.

The paper, written by a large group of Chinese researchers from several institutions, offers details about the first 41 hospitalized patients who had confirmed infections with what has been dubbed 2019 novel coronavirus (2019-nCoV). In the earliest case, the patient became ill on 1 December 2019 and had no reported link to the seafood market, the authors report. “No epidemiological link was found between the first patient and later cases,” they state. [Their data also show that, in total, 13 of the 41 cases had no link to the marketplace.](#) “That’s a big number, 13, with no link,” says Daniel Lucey, an infectious disease specialist at Georgetown University.

SARS

Spread of Sars epidemic in 2002-3



Number of probable cases Nov 2002-Jul 2003



Source: WHO



Discovery of a rich gene pool of bat SARS-related coronaviruses provides new insights into the origin of SARS coronavirus

Ben Hu , Lei-Ping Zeng , Xing-Lou Yang , Xing-Yi Ge, Wei Zhang, Bei Li, Jia-Zheng Xie, Xu-Rui Shen, Yun-Zhi Zhang, Ning Wang, Dong-Sheng Luo, Xiao-Shuang Zheng, Mei-Niang Wang, [...], Zheng-Li Shi  [view all]

Published: November 30, 2017 • <https://doi.org/10.1371/journal.ppat.1006698>

“Herein, we report the identification of a diverse group of bat SARSr-CoVs in a single cave in Yunnan, China. Importantly, all of the building blocks of SARS-CoV genome, including the highly variable S gene, ORF8 and ORF3, could be found in the genomes of different SARSr-CoV strains from this single location.”

- Hu et al. 2017

“In their paper, the Chinese team warn that another deadly outbreak of Sars could emerge at any time. As they point out, the cave where they discovered their strain is only a kilometre from the nearest village.”

- *The Guardian* coverage of Hu et al. 2017

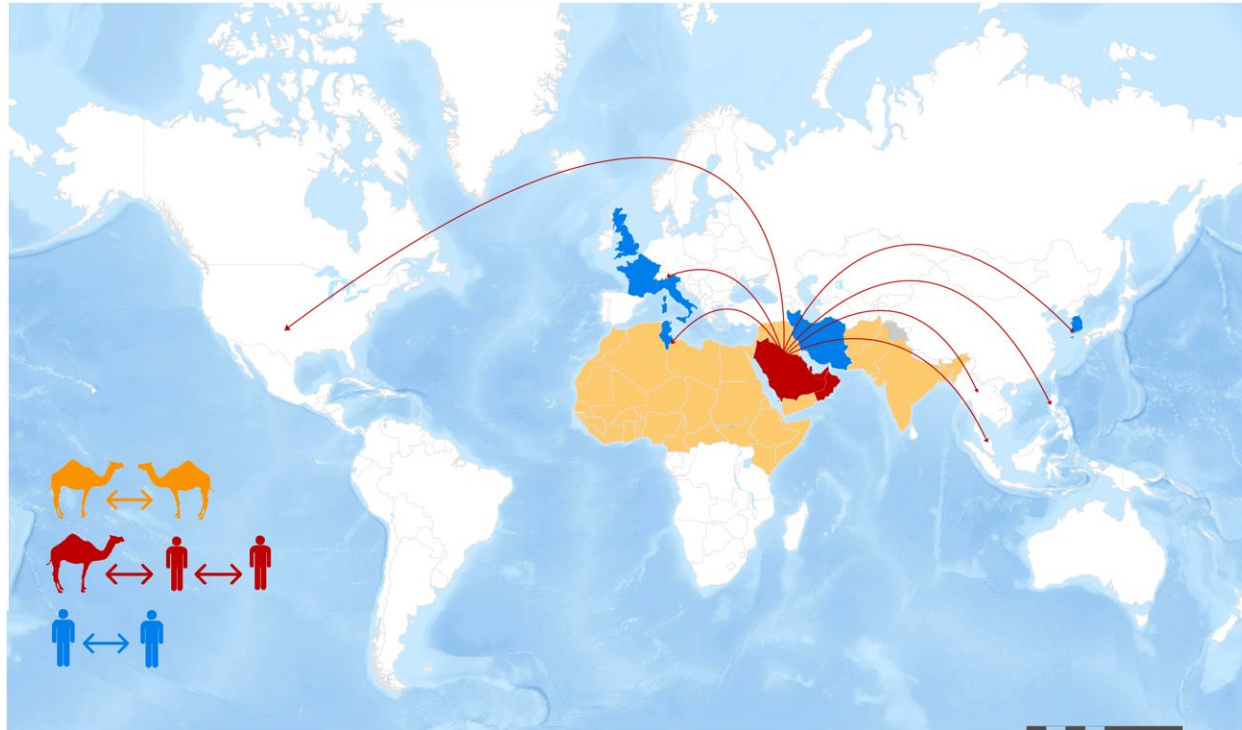
MERS

MERS-COV TRANSMISSION AND GEOGRAPHIC RANGE



World Health
Organization

MAP DATE: 19 January 2018



Data Source: World Health Organization
Map Production: WHO Health Emergencies Programme

The boundaries and names shown and the designations used on this map do not imply the expression of any opinion whatsoever on the part of the World Health Organization concerning the legal status of any country, territory, city or area or of its authorities, or concerning the delimitation of its frontiers or boundaries. Dotted and dashed lines on maps represent approximate border lines for which there may not yet be full agreement.

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A pneumonia outbreak associated with a new coronavirus of probable bat origin

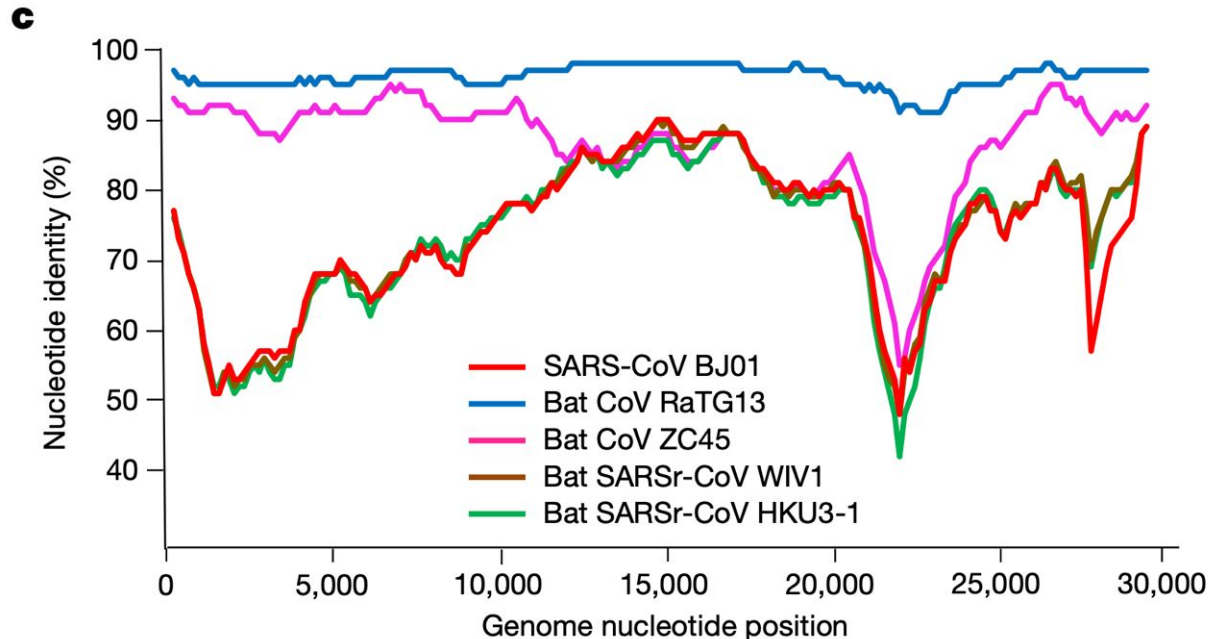
<https://doi.org/10.1038/s41586-020-2012-7>

Received: 20 January 2020

Accepted: 29 January 2020

Published online: 3 February 2020

Peng Zhou^{1,5}, Xing-Lou Yang^{1,5}, Xian-Guang Wang^{2,5}, Ben Hu¹, Lei Zhang¹, Wei Zhang¹, Hao-Rui Si^{1,3}, Yan Zhu¹, Bei Li¹, Chao-Lin Huang², Hui-Dong Chen², Jing Chen^{1,3}, Yun Luo^{1,3}, Hua Guo^{1,3}, Ren-Di Jiang^{1,3}, Mei-Qin Liu^{1,3}, Ying Chen^{1,3}, Xu-Rui Shen^{1,3}, Xi Wang^{1,3}, Xiao-Shuang Zheng^{1,3}, Kai Zhao^{1,3}, Quan-Jiao Chen¹, Fei Deng¹, Lin-Lin Liu⁴, Bing Yan¹, Fa-Xian Zhan⁴, Yan-Yi Wang¹, Geng-Fu Xiao¹ & Zheng-Li Shi^{1,2,5}



Where does that leave us with SARS-CoV-2?

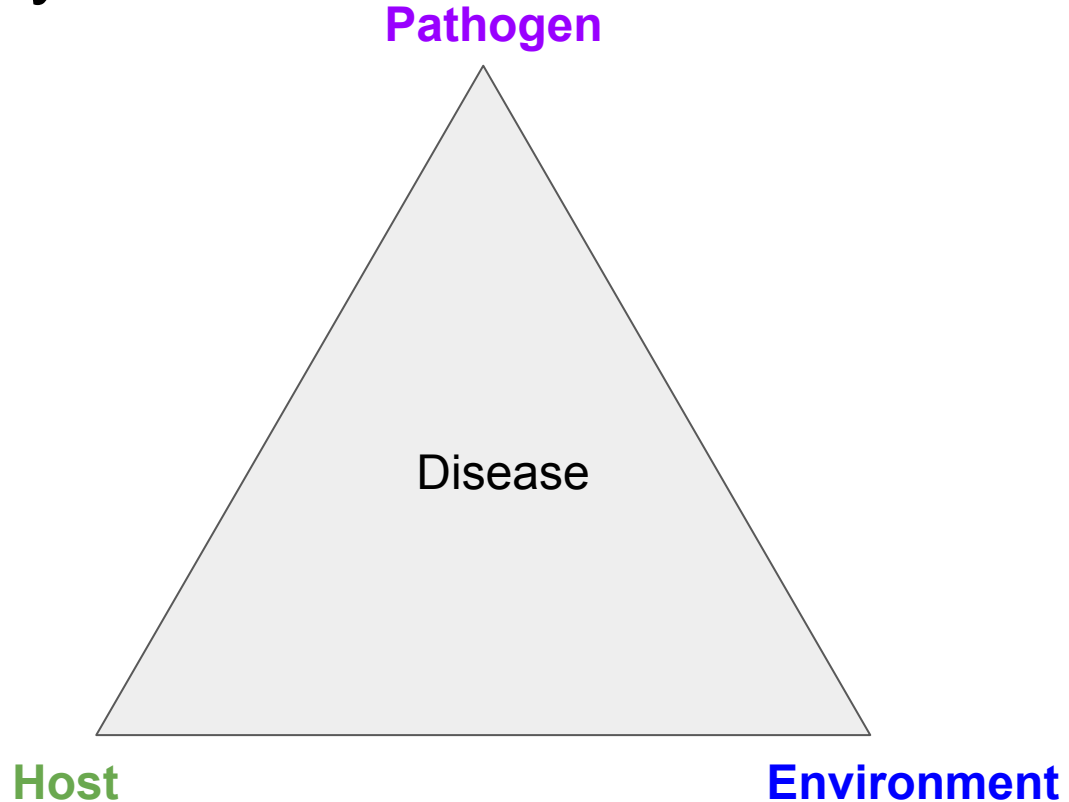
- We may never be able to precisely identify the initial spillover event
- Viral surveillance in wildlife can get us closer to understanding viral diversity in natural hosts (one clue)
- Viral surveillance in humans (especially serosurveys) can highlight populations where spillover may be relatively frequent but previously undetected (another clue)



Disease Triangle Activity

Using the google slides link in the chat window:

Brainstorm as many factors specific to each of these three categories (Pathogen, Host, and Environment) that may impact the COVID-19 Pandemic.



Disease Triangle COVID-19

Host specific factors include...

- Handwashing
- Staying home if symptomatic
- Immune response
- Race/Ethnicity
- Age
- Genetics
- Sleep
- Nutrition

Host

Pathogen

COVID-19

Pathogen specific factors include...

- Mutation rate
- Accumulation of mutations
- Route of entry
- Pathogen structure impacts which disinfectants are effective
- Pathogen structure/function impacts which treatments are effective

Environment specific factors include...

- Mask compliance
- Physical distancing
- Climate
- Natural disasters
- Healthcare availability
- Testing availability
- Contact tracing

Environment